RAW SEQUENCE LISTING   DATE: 10/27/2003
PATENT APPLICATION: US/09/595,947D   TIME: 09:29:14

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\10272003\I595947D.raw

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  5 <110> APPLICANT: ICARD-LIEPKALNS, Christine
  6        MALLET, Jacques
  7        RAVASSARD, Philippe
  9 <120> TITLE OF INVENTION: POLYPEPTIDES OF THE "BASIC-HELIX-LOOP-HELIX" bHLH
 10        FAMILY, CORRESPONDING NUCLEIC ACID SEQUENCES
 12 <130> FILE REFERENCE: P26,952 USA
 14 <140> CURRENT APPLICATION NUMBER: US 09/595,947D
 15 <141> CURRENT FILING DATE: 2000-06-16
 17 <150> PRIOR APPLICATION NUMBER: FR96/15651
 18 <151> PRIOR FILING DATE: 1996-12-19
 20 <150> PRIOR APPLICATION NUMBER: PCT/FR97/02368
 21 <151> PRIOR FILING DATE: 1997-12-19
 23 <150> PRIOR APPLICATION NUMBER: US 09/331,356
 24 <151> PRIOR FILING DATE: 1999-07-12
 26 <160> NUMBER OF SEQ ID NOS: 40
 28 <170> SOFTWARE: PatentIn Ver. 3.1
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ERRORED SEQUENCES

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129 <210> SEQ ID NO: 5
130 <211> LENGTH: 18
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
135 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primers
137 <400> SEQUENCE: 5 cgcggtgtcc tgcccacc 18
E--> 137 5 cgcggtgtcc tgcccacc 18
164 <210> SEQ ID NO: 8
165 <211> LENGTH: 214
166 <212> TYPE: PRT
167 <213> ORGANISM: Rattus norvegicus
169 <400> SEQUENCE: 8
170 Met Ala Pro His Pro Leu Asp Ala Pro Thr Ile Gln Val Ser Gln Glu
171 1               5               10              15
173 Thr Gln Gln Pro Phe Pro Gly Ala Ser Asp His Glu Val Leu Ser Ser
174             20              25              30
176 Asn Ser Thr Pro Pro Ser Pro Thr Leu Val Pro Arg Asp Cys Ser Glu
177         35              40              45
179 Ala Glu Ala Gly Asp Cys Arg Gly Thr Ser Arg Lys Leu Arg Ala Arg
180     50              55              60
182 Arg Gly Gly Arg Asn Arg Pro Lys Ser Glu Leu Ala Leu Ser Lys Gln
183 65              70              75              80
```

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```
         185 Arg Arg Ser Arg Arg Lys Lys Ala Asn Asp Arg Glu Arg Asn Arg Met
         186             85              90                  95
E--> 188 His Asn Leu Asn Ser Ala Leu Asp Ala Leu Arg Gly Val Leu Pro Thr
E--> 189             100             105                 110
         191 Phe Pro Asp Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala
E--> 192             115             120                 125
         194 His Asn Tyr Ile Trp Ala Leu Thr Gln Thr Leu Arg Ile Ala Asp His
E--> 195             130             135                 140
         197 Ser Phe Tyr Gly Pro Glu Pro Pro Val Pro Cys Gly Glu Leu Gly Ser
E--> 198 145             150                 155                 160
         200 Pro Gly Gly Gly Ser Ser Gly Asp Trp Gly Ser Ile Tyr Ser Pro Val
E--> 201             165                 170                 175
         203 Ser Gln Ala Gly Ser Leu Ser Pro Thr Ala Ser Leu Glu Glu Phe Pro
E--> 204             180                 185                 190
         206 Gly Leu Gln Val Pro Ser Ser Pro Ser Cys Leu Leu Pro Gly Thr Leu
E--> 207             195                 200                 205
         209 Val Phe Ser Asp Phe Leu
E--> 210             210
         266 <210> SEQ ID NO: 10
         267 <211> LENGTH: 214
         268 <212> TYPE: PRT
         269 <213> ORGANISM: Homo sapiens
         271 <400> SEQUENCE: 10
         272 Met Thr Pro Gln Pro Ser Gly Ala Pro Thr Val Gln Val Thr Arg Glu
         273  1               5               10                  15
         275 Thr Glu Arg Ser Phe Pro Arg Ala Ser Glu Asp Glu Val Thr Cys Pro
         276             20              25                  30
         278 Thr Ser Ala Pro Pro Ser Pro Thr Arg Thr Pro Gly Asn Cys Ala Glu
         279             35              40                  45
         281 Ala Glu Glu Gly Gly Cys Arg Gly Ala Pro Arg Lys Leu Arg Ala Arg
         282             50              55                  60
         284 Arg Gly Gly Arg Ser Arg Pro Lys Ser Glu Leu Ala Leu Ser Lys Gln
         285  65              70                  75                  80
         287 Arg Arg Ser Arg Arg Lys Lys Ala Asn Asp Arg Glu Arg Asn Arg Met
         288             85              90                  95
         290 His Asp Leu Asn Ser Ala Leu Asp Ala Leu Arg Gly Val Leu Pro Thr
         291             100             105                 110
         293 Phe Pro Asp Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala
         294             115             120                 125
         296 His Asn Tyr Ile Trp Ala Leu Thr Gln Thr Leu Arg Ile Ala Asp His
         297             130             135                 140
E--> 299 Ser Leu Tyr Ala Leu Glu Pro Pro Ala Pro His Cys Gly Glu Leu Gly
         300 145             150                 155                 160
         302 Ser Pro Gly Gly Pro Pro Gly Asp Trp Gly Ser Leu Tyr Ser Pro Val
         303             165                 170                 175
         304 Ser Gln Ala Gly Ser Leu Ser Pro Ala Ala Ser Leu Glu Glu Arg Pro
         305             180                 185                 190
         307 Gly Leu Leu Gly Ala Thr Ser Ser Ala Cys Leu Ser Pro Gly Ser Leu
         308             195                 200                 205
```

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       Input Set : A:\PTO.KD.txt
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310 Ala Phe Ser Asp Phe Leu
311   · 210

<210> 8
<211> 214
<212> PRT
<213> Rattus norvegicus

<400> 8
Met Ala Pro His Pro Leu Asp Ala Pro Thr Ile Gln Val Ser Gln Glu
1   5   10   15

Thr Gln Gln Pro Phe Pro Gly Ala Ser Asp His Glu Val Leu Ser Ser
                20   25   30

Asn Ser Thr Pro Pro Ser Pro Thr Leu Val Pro Arg Asp Cys Ser Glu
            35   40   45

Ala Glu Ala Gly Asp Cys Arg Gly Thr Ser Arg Lys Leu Arg Ala Arg
        50   55   60

Arg Gly Gly Arg Asn Arg Pro Lys Ser Glu Leu Ala Leu Ser Lys Gln
65   70   75   80

Arg Arg Ser Arg Arg Lys Lys Ala Asn Asp Arg Glu Arg Asn Arg Met
            85   90   95

His Asn Leu Asn Ser Ala Leu Asp Ala Leu Arg Gly Val Leu Pro Thr
            100   105   110

<210> 13
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 13
atcgttgaga ctcgtaccag cagagtcacg agagagacta cacggtactg gnnnnnnnnn 60

see p. 6 for error explanation

Input Set : A:\PTO.KD.txt
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error Explanation

Use of n's or Xaa's(NEW_RULES):
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n!s or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:2; N Pos. 9,16
Seq#:13; N Pos. 52,53,54,55,56,57,58,59,60

see p. 7 for more error

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\10272003\I595947D.raw**

L:100 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:2
L:100 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:2
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:137 M:301 E: (44) No Sequence Data was Shown, SEQ ID:5
L:137 M:252 E: No. of Seq. differs, <211> LENGTH:Input:18 Found:0 SEQ:5
L:188 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:189 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
M:332 Repeated in SeqNo=8
L:210 M:252 E: No. of Seq. differs, <211> LENGTH:Input:214 Found:213 SEQ:8
L:299 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:347 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:13
L:347 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:13
L:347 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:499 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:501 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:26, <213>
ORGANISM:Artificial Sequence
L:501 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:26,Line#:501
L:510 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:512 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:27, <213>
ORGANISM:Artificial Sequence
L:512 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:512